

CRF Errors Corrected by the STIC System Branch

Serial Number: 10/019,375

Processing Date: 1/29/2002

Edited by: A  
Verified by: A (STIC staff)

**ENTERED**

*P4/10 50 L1*  
*#3*

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



PCT10

## RAW SEQUENCE LISTING

DATE: 01/27/2002

PATENT APPLICATION: US/10/019,595

TIME: 19:46:16

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01272002\J019595.raw

PS

```

5 <110> APPLICANT: Brett P. Monia
6      William Gaarde
7      Lex M. Cowsert
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK5 EXPRESSION
11 <130> FILE REFERENCE: RTSP-0265
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/019,595
C--> 13 <141> CURRENT FILING DATE: 2001-12-26
13 <150> PRIOR APPLICATION NUMBER: 09/359,757
14 <151> PRIOR FILING DATE: 1999-07-23
16 <160> NUMBER OF SEQ ID NOS: 47
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 5236
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (361)..(4485)
27 <220> FEATURE:
28 <221> NAME/KEY: unsure
29 <222> LOCATION: 4687
30 <223> OTHER INFORMATION: unknown
32 <400> SEQUENCE: 1
33 cgagcgcggc gcccttgagc tgcaccgcgg cgaggtttg cgagccgact tgtcagccgg 60
35 ccaagaaaag gaagctccgt cccttccgc tcaccgggt tccccacccc ttgtactcta 120
37 aactctgcac agggcgagcg ggcgggccac tgatgcgcgg aggaggagcg agccgcgcgc 180
39 gggcagcggc gtgccctcgg gggagagggc gccggataag agcggcggcg cggcggcgat 240
41 ggcgcggcgc gcgatggcag ctgcttagcc cggcgggcgc ggagcagccc cgagctgtgg 300
43 ctggccaggc ggtgcggctg ggcgggggac gccgcgcgcg ttgctgccg gcccgagag 360
45 atg agc acg gag gcg gac gaa ggc atc act ttc tct gtg cca ccc ttc 408
46 Met Ser Thr Glu Ala Asp Glu Gly Ile Thr Phe Ser Val Pro Pro Phe
47 1          5          10          15
49 gcc ccc tcg ggc ttc tgc acc atc ccc gag ggc ggc atc tgc agg agg 456
50 Ala Pro Ser Gly Phe Cys Thr Ile Pro Glu Gly Gly Ile Cys Arg Arg
51          20          25          30
53 gga gga gcg gcg gcg gtg ggc gag ggc gag gag cac cag ctg cca ccg 504
54 Gly Gly Ala Ala Val Gly Glu Gly Glu Glu His Gln Leu Pro Pro
55          35          40          45
57 ccg ccg ccg ggc agc ttc tgg aac gtg gag agc gcc gct gcc cct ggc 552
58 Pro Pro Pro Gly Ser Phe Trp Asn Val Glu Ser Ala Ala Ala Pro Gly
59          50          55          60
61 atc ggt tgt ccg gcg gcc acc tcc tcg agc agt gcc acc cga ggc cgg 600
62 Ile Gly Cys Pro Ala Ala Thr Ser Ser Ser Ala Thr Arg Gly Arg
63 65          70          75          80

```

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```

65 ggc agc tct gtt ggc ggg ggc agc cga cgg acc acg gtg gca tat gtg      648
66 Gly Ser Ser Val Gly Gly Gly Ser Arg Arg Thr Thr Val Ala Tyr Val
W--> 67 85          90          95          100
69 atc aac gaa gcg agc caa ggg caa ctg gtg gtg gcc gag agc gag gcc      696
70 Ile Asn Glu Ala Ser Gln Gly Gln Leu Val Val Ala Glu Ser Glu Ala
W--> 71          105          110          115
73 ctg cag agc ttg cgg gag gcg tgc gag aca gtg ggc gcc acc ctg gaa      744
74 Leu Gln Ser Leu Arg Glu Ala Cys Glu Thr Val Gly Ala Thr Leu Glu
W--> 75          120          125          130
77 acc ctg cat ttt ggg aaa ctc gac ttt gga gaa acc acc gtg ctg gac      792
78 Thr Leu His Phe Gly Lys Leu Asp Phe Gly Glu Thr Thr Val Leu Asp
W--> 79          135          140          145
81 cgc ttt tac aat gca gat att gcg glg gtg gag atg agc gat gcc ttc      840
82 Arg Phe Tyr Asn Ala Asp Ile Ala Val Val Glu Met Ser Asp Ala Phe
W--> 83          150          155          160
85 cgg cag ccg tcc ttg ttt tac cac ctt ggg gtg aga gaa agt ttc agc      888
86 Arg Gln Pro Ser Leu Phe Tyr His Leu Gly Val Arg Glu Ser Phe Ser
W--> 87 165          170          175          180
89 atg gcc aac aac atc atc ctc tac tgt gat act aac tcg gac tct ctg      936
90 Met Ala Asn Asn Ile Ile Leu Tyr Cys Asp Thr Asn Ser Asp Ser Leu
W--> 91          185          190          195
93 cag tca ctg aag gaa ata att tgc cag aag aat act atg tgc act ggg      984
94 Gln Ser Leu Lys Glu Ile Ile Cys Gln Lys Asn Thr Met Cys Thr Gly
W--> 95          200          205          210
97 aac tac acc ttt gtt cct tac atg ata act cca cat aac aaa gtc tac      1032
98 Asn Tyr Thr Phe Val Pro Tyr Met Ile Thr Pro His Asn Lys Val Tyr
W--> 99          215          220          225
101 tgc tgt gac agc agc ttc atg aag ggg ttg aca gag ctc atg caa ccg      1080
102 Cys Cys Asp Ser Ser Phe Met Lys Gly Leu Thr Glu Leu Met Gln Pro
W--> 103 230          235          240          245
105 aac ttc gag ctg ctt ctt gga ccc atc tgc tta cct ctt gtg gat cgt      1128
106 Asn Phe Glu Leu Leu Gly Pro Ile Cys Leu Pro Leu Val Asp Arg
W--> 107          250          255          260
109 ttt att caa ctt ttg aag gtg gca caa gca agt tct agc cag tac ttc      1176
110 Phe Ile Gln Leu Leu Lys Val Ala Gln Ala Ser Ser Ser Gln Tyr Phe
W--> 111          265          270          275
113 cgg gaa tct ata ctc aat gac atc agg aaa gct cgt aat tta tac act      1224
114 Arg Glu Ser Ile Leu Asn Asp Ile Arg Lys Ala Arg Asn Leu Tyr Thr
W--> 115          280          285          290
117 ggt aaa gaa ttg gca gct gag ttg gca aga att cgg cag cga gta gat      1272
118 Gly Lys Glu Leu Ala Ala Glu Leu Ala Arg Ile Arg Gln Arg Val Asp
W--> 119          295          300          305
121 aat atc gaa gtc ttg aca gca gat att gtc ata aat ctg tta ctt tcc      1320
122 Asn Ile Glu Val Leu Thr Ala Asp Ile Val Ile Asn Leu Leu Leu Ser
123 305          310          315          320
125 tac aga gat atc cag gac tat gat tct att gtg aag ctg gta gag act      1368
126 Tyr Arg Asp Ile Gln Asp Tyr Asp Ser Ile Val Lys Leu Val Glu Thr
127          325          330          335
129 tta gaa aaa ctg cca acc ttt gat ttg gcc tcc cat cac cat gtg aag      1416

```

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130	Leu	Glu	Lys	Leu	Pro	Thr	Phe	Asp	Leu	Ala	Ser	His	His	His	Val	Lys	
131				340					345					350			
133	ttt	cat	tat	gca	ttt	gca	ctg	aat	agg	aga	aat	ctc	cct	ggt	gac	aga	1464
134	Phe	His	Tyr	Ala	Phe	Ala	Leu	Asn	Arg	Arg	Asn	Leu	Pro	Gly	Asp	Arg	
135			355					360					365				
137	gca	aaa	gct	ctt	gat	att	atg	att	ccc	atg	gtg	caa	agc	gaa	gga	caa	1512
138	Ala	Lys	Ala	Leu	Asp	Ile	Met	Ile	Pro	Met	Val	Gln	Ser	Glu	Gly	Gln	
139		370					375					380					
141	gtt	gct	tca	gat	atg	tat	tgc	cta	gtt	ggt	cga	atc	tac	aaa	gat	atg	1560
142	Val	Ala	Ser	Asp	Met	Tyr	Cys	Leu	Val	Gly	Arg	Ile	Tyr	Lys	Asp	Met	
143	385					390				395					400		
145	ttt	ttg	gac	tct	aat	ttc	acg	gac	act	gaa	agc	aga	gac	cat	gga	gct	1608
146	Phe	Leu	Asp	Ser	Asn	Phe	Thr	Asp	Thr	Glu	Ser	Arg	Asp	His	Gly	Ala	
147				405					410					415			
149	tct	tgg	ttc	aaa	aag	gca	ttt	gaa	tct	gag	cca	aca	cta	cag	tca	gga	1656
150	Ser	Trp	Phe	Lys	Lys	Ala	Phe	Glu	Ser	Glu	Pro	Thr	Leu	Gln	Ser	Gly	
151			420					425					430				
153	att	aat	tat	gcg	gtc	ctc	ctc	ctg	gca	gct	gga	cac	cag	ttt	gaa	tct	1704
154	Ile	Asn	Tyr	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly	His	Gln	Phe	Glu	Ser	
155		435					440					445					
157	tcc	ttt	gag	ctc	cgg	aaa	gtt	ggg	gtg	aag	cta	agt	agt	ctt	ctt	ggt	1752
158	Ser	Phe	Glu	Leu	Arg	Lys	Val	Gly	Val	Lys	Leu	Ser	Ser	Leu	Leu	Gly	
159		450				455					460						
161	aaa	aag	gga	aac	ttg	gaa	aaa	ctc	cag	agc	tac	tgg	gaa	gtt	gga	ttt	1800
162	Lys	Lys	Gly	Asn	Leu	Glu	Lys	Leu	Gln	Ser	Tyr	Trp	Glu	Val	Gly	Phe	
163	465				470				475					480			
165	ttt	ctg	ggg	gcc	agc	gtc	cta	gcc	aat	gac	cac	atg	aga	gtc	att	caa	1848
166	Phe	Leu	Gly	Ala	Ser	Val	Leu	Ala	Asn	Asp	His	Met	Arg	Val	Ile	Gln	
167			485					490					495				
169	gca	tct	gaa	aag	ctt	ttt	aaa	ctg	aag	aca	cca	gca	tgg	tac	ctc	aag	1896
170	Ala	Ser	Glu	Lys	Leu	Phe	Lys	Leu	Lys	Thr	Pro	Ala	Trp	Tyr	Leu	Lys	
171		500						505					510				
173	tct	att	gta	gag	aca	att	tta	ata	tat	aag	cat	ttt	gtg	aaa	ctg	acc	1944
174	Ser	Ile	Val	Glu	Thr	Ile	Leu	Ile	Tyr	Lys	His	Phe	Val	Lys	Leu	Thr	
175		515					520					525					
177	aca	gaa	cag	cct	gtg	gcc	aag	caa	gaa	ctt	gtg	gac	ttt	tgg	atg	gat	1992
178	Thr	Glu	Gln	Pro	Val	Ala	Lys	Gln	Glu	Leu	Val	Asp	Phe	Trp	Met	Asp	
179		530				535					540						
181	ttc	ctg	gtc	gag	gcc	aca	aag	aca	gat	gtt	act	gtg	gtt	agg	ttt	cca	2040
182	Phe	Leu	Val	Glu	Ala	Thr	Lys	Thr	Asp	Val	Thr	Val	Val	Arg	Phe	Pro	
183	545				550					555				560			
185	gta	tta	ata	tta	gaa	cca	acc	aaa	atc	tat	caa	cct	tct	tat	ttg	tct	2088
186	Val	Leu	Ile	Leu	Glu	Pro	Thr	Lys	Ile	Tyr	Gln	Pro	Ser	Tyr	Leu	Ser	
187			565					570					575				
189	atc	aac	aat	gaa	gtt	gag	gaa	aag	aca	atc	tct	att	tgg	cac	gtg	ctt	2136
190	Ile	Asn	Asn	Glu	Val	Glu	Glu	Lys	Thr	Ile	Ser	Ile	Trp	His	Val	Leu	
191			580					585					590				
193	cct	gat	gac	aag	aaa	ggt	ata	cat	gag	tgg	aat	ttt	agt	gcc	tct	tct	2184
194	Pro	Asp	Asp	Lys	Lys	Gly	Ile	His	Glu	Trp	Asn	Phe	Ser	Ala	Ser	Ser	

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195	595	600	605	
197	gtc agg gga gtg agt att tct aaa ttt gaa gaa aga tgc tgc ttt ctt	2232		
198	Val Arg Gly Val Ser Ile Ser Lys Phe Glu Glu Arg Cys Cys Phe Leu			
199	610 615 620			
201	tat gtg ctt cac aat tct gat gat ttc caa atc tat ttc tgt aca gaa	2280		
202	Tyr Val Leu His Asn Ser Asp Asp Phe Gln Ile Tyr Phe Cys Thr Glu			
203	625 630 635 640			
205	ctt cat tgt aaa aag ttt ttt gag atg gtg aac acc att acc gaa gag	2328		
206	Leu His Cys Lys Lys Phe Phe Glu Met Val Asn Thr Ile Thr Glu Glu			
207	645 650 655			
209	aag ggg aga agc aca gag gaa gga gac tgt gaa agt gac ttg ctg gag	2376		
210	Lys Gly Arg Ser Thr Glu Glu Gly Asp Cys Glu Ser Asp Leu Leu Glu			
211	660 665 670			
213	tat gac tat gaa tat gat gaa aat ggt gac aga gtc gtt tta gga aaa	2424		
214	Tyr Asp Tyr Glu Tyr Asp Glu Asn Gly Asp Arg Val Val Leu Gly Lys			
215	675 680 685			
217	ggc act tat ggg ata gtc tac gca ggt cgg gac ttg agc aac caa gtc	2472		
218	Gly Thr Tyr Gly Ile Val Tyr Ala Gly Arg Asp Leu Ser Asn Gln Val			
219	690 695 700			
221	aga att gct att aag gaa atc cca gag aga gac agc aga tac tct cag	2520		
222	Arg Ile Ala Ile Lys Glu Ile Pro Glu Arg Asp Ser Arg Tyr Ser Gln			
223	705 710 715 720			
225	ccc ctg cat gaa gaa ata gca ttg cat aaa cac ctg aag cac aaa aat	2568		
226	Pro Leu His Glu Glu Ile Ala Leu His Lys His Leu Lys His Lys Asn			
227	725 730 735			
229	att gtc cag tat ctg ggc tct ttc agt gag aat ggt ttc att aaa atc	2616		
230	Ile Val Gln Tyr Leu Gly Ser Phe Ser Glu Asn Gly Phe Ile Lys Ile			
231	740 745 750			
233	ttc atg gag cag gtc cct gga gga agt ctt tct gct ctc ctt cgt tcc	2664		
234	Phe Met Glu Gln Val Pro Gly Gly Ser Leu Ser Ala Leu Leu Arg Ser			
235	755 760 765			
237	aaa tgg ggt cca tta aaa gac aat gag caa aca att ggc ttt tat aca	2712		
238	Lys Trp Gly Pro Leu Lys Asp Asn Glu Gln Thr Ile Gly Phe Tyr Thr			
239	770 775 780			
241	aag caa ata ctg gaa gga tta aaa tat ctc cat gac aat cag ata gtt	2760		
242	Lys Gln Ile Leu Glu Gly Leu Lys Tyr Leu His Asp Asn Gln Ile Val			
243	785 790 795 800			
245	cac cgg gac ata aag ggt gac aat gtg ttg att aat acc tac agt ggt	2808		
246	His Arg Asp Ile Lys Gly Asp Asn Val Leu Ile Asn Thr Tyr Ser Gly			
247	805 810 815			
249	gtt ctc aag atc tct gac ttc gga aca tca aag agg ctt gct ggc ata	2856		
250	Val Leu Lys Ile Ser Asp Phe Gly Thr Ser Lys Arg Leu Ala Gly Ile			
251	820 825 830			
253	aac ccc tgt act gaa act ttt act ggt acc ctc cag tat atg gca cca	2904		
254	Asn Pro Cys Thr Glu Thr Phe Thr Gly Thr Leu Gln Tyr Met Ala Pro			
255	835 840 845			
257	gaa ata ata gat aaa gga cca aga ggc tac gga aaa gca gca gac atc	2952		
258	Glu Ile Ile Asp Lys Gly Pro Arg Gly Tyr Gly Lys Ala Ala Asp Ile			
259	850 855 860			

## RAW SEQUENCE LISTING

DATE: 01/27/2002

PATENT APPLICATION: US/10/019,595

TIME: 19:46:16


Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01272002\J019595.raw

```

261 tgg tct ctg ggc tgt aca atc att gaa atg gcc aca gga aaa ccc cca 3000
262 Trp Ser Leu Gly Cys Thr Ile Ile Glu Met Ala Thr Gly Lys Pro Pro
263 865 870 875 880
265 ttt tat gaa ctg gga gaa cca caa gca gct atg ttc aag gtg gga atg 3048
266 Phe Tyr Glu Leu Gly Glu Pro Gln Ala Ala Met Phe Lys Val Gly Met
267 885 890 895
269 ttt aaa gtc cac cct gag atc cca gag tcc atg tct gca gag gcc aag 3096
270 Phe Lys Val His Pro Glu Ile Pro Glu Ser Met Ser Ala Glu Ala Lys
271 900 905 910
273 gca ttc ata ctg aaa tgt ttt gaa cca gat cct gac aag aga gcc tgt 3144
274 Ala Phe Ile Leu Lys Cys Phe Glu Pro Asp Pro Asp Lys Arg Ala Cys
275 915 920 925
277 gct aac gac ttg ctt gtt gat gag ttt tta aaa gtt tca agc aaa aag 3192
278 Ala Asn Asp Leu Leu Val Asp Glu Phe Leu Lys Val Ser Ser Lys Lys
279 930 935 940
281 aaa aag aca caa cct aag ctt tca gct ctt tca gct gga tca aat gaa 3240
282 Lys Lys Thr Gln Pro Lys Leu Ser Ala Leu Ser Ala Gly Ser Asn Glu
283 945 950 955 960
285 tat ctc agg agt ata tcc ttg ccg gta cct gtg ctg gtg gag gac acc 3288
286 Tyr Leu Arg Ser Ile Ser Leu Pro Val Pro Val Leu Val Glu Asp Thr
287 965 970 975
289 agc agc agc agt gag tac ggc tca gtt tca ccc gac acg gag ttg aaa 3336
290 Ser Ser Ser Ser Glu Tyr Gly Ser Val Ser Pro Asp Thr Glu Leu Lys
291 980 985 990
293 gtg gac ccc ttc tct ttc aaa aca aga gcc aag tcc tgc gga gaa aga 3384
294 Val Asp Pro Phe Ser Phe Lys Thr Arg Ala Lys Ser Cys Gly Glu Arg
295 995 1000 1005
297 gat gtc aag gga att cgg aca ctc ttt ttg ggc att cca gat gag aat 3432
298 Asp Val Lys Gly Ile Arg Thr Leu Phe Leu Gly Ile Pro Asp Glu Asn
299 1010 1015 1020
301 ttt gaa gat cac agt gct cct cct tcc cct gaa gaa aaa gat tct gga 3480
302 Phe Glu Asp His Ser Ala Pro Pro Ser Pro Glu Glu Lys Asp Ser Gly
303 1025 1030 1035 1040
305 ttc ttc atg ctg agg aag gac agt gag agg cga gct acc ctt cac agg 3528
306 Phe Phe Met Leu Arg Lys Asp Ser Glu Arg Arg Ala Thr Leu His Arg
307 1045 1050 1055
309 atc ctg acg gaa gac caa gac aaa att gtg aga aac cta atg gaa tct 3576
310 Ile Leu Thr Glu Asp Gln Asp Lys Ile Val Arg Asn Leu Met Glu Ser
311 1060 1065 1070
313 tta gct cag ggg gct gaa gaa ccg aaa cta aaa tgg gaa cac atc aca 3624
314 Leu Ala Gln Gly Ala Glu Glu Pro Lys Leu Lys Trp Glu His Ile Thr
315 1075 1080 1085
317 acc ctc att gca agc ctc aga gaa ttt gtg aga tcc act gac cga aaa 3672
318 Thr Leu Ile Ala Ser Leu Arg Glu Phe Val Arg Ser Thr Asp Arg Lys
319 1090 1095 1100
321 atc ata gcc acc aca ctg tca aag ctg aaa ctg gag ctg gac ttc gac 3720
322 Ile Ile Ala Thr Thr Leu Ser Lys Leu Lys Leu Glu Leu Asp Phe Asp
323 1105 1110 1115 1120
325 agc cat ggc att agc caa gtc cag gtg gta ctc ttt ggt ttt caa gat 3768

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 If a n and/or Xaa has been detected in the Sequence Listing,  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 01/27/2002

PATENT APPLICATION: US/10/019,595

TIME: 19:46:17

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01272002\J019595.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1



PCT10

## RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/10/019,595

TIME: 10:37:36

Input Set : A:\rtsp-265sequence.txt

Output Set: N:\CRF3\01182002\J019595.raw

**Does Not Comply**  
**Corrected Diskette Needed**

5 <110> APPLICANT: Brett P. Monia  
 6 William Gaarde  
 7 Lex M. Cowser  
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK5 EXPRESSION  
 11 <130> FILE REFERENCE: RTSP-0265  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/019,595  
 C--> 13 <141> CURRENT FILING DATE: 2001-12-26  
 13 <150> PRIOR APPLICATION NUMBER: 09/359,757  
 14 <151> PRIOR FILING DATE: 1999-07-23  
 16 <160> NUMBER OF SEQ ID NOS: 47

## ERRORED SEQUENCES

957 <210> SEQ ID NO: 47  
 958 <211> LENGTH: 20  
 959 <212> TYPE: DNA  
 960 <213> ORGANISM: Artificial Sequence  
 962 <220> FEATURE:  
 963 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 965 <400> SEQUENCE: 47  
 966 gcacgatcac atgaatgta  
 E--> 968 1  
 E--> 971 17 *delete*

20

## VERIFICATION SUMMARY

DATE: 01/22/2002

PATENT APPLICATION: US/10/019,595

TIME: 10:37:37

Input Set : A:\rtsp-265sequence.txt

Output Set: N:\CRF3\01182002\J019595.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:1  
L:968 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:47  
M:254 Repeated in SeqNo=47